Remarks

Claims 39-64 have been added, and claims 4-7 and 28-38 have been amended without prejudice. It is noted that claims 1-3 were canceled without prejudice as directed to a non-elected invention. Regardless, Applicants reserve the right to prosecute the non-elected invention in a continuing application. As such, claims 4-7 and 28-64 are pending after entry of the present amendment. No new matter enters by way of the present amendment. Support for the foregoing claim amendments may be found throughout the specification, and in the original claims. Specifically, support can be found, for example, at page 1, lines 15 through page 2, line 21; page 21, lines 4-26; page 22, lines 10-29; page 28, lines 1 – 29; page 29, lines 6-19; page 31, lines 1-18; and Figures 4, 6, 7, 11, and 12 of the specification as filed.

In response to the Examiner's objection to the drawings, it is noted that the substitute Figure 12 previously submitted on April 16, 2002 is not color. As such, the Examiner's comment regarding color appears inapplicable. If this does not fully address the Examiner's concern regarding the drawings, clarification is requested.

I. Rejections Under 35 U.S.C. 112, Second Paragraph

Claims 30-38 stand rejected under 35 U.S.C. § 112, second paragraph, for purportedly being indefinite. According to the Examiner, the claims are indefinite in that it is unclear as to the reference sequence to which the amino acid substitution has been incorporated. Office Action mailed March 6, 2003 at page 3. Although Applicants disagree with the rejection, the rejected claims have been amended without prejudice to facilitate prosecution. By the present amendment, the claims have been amended to recite a substitution of at least one amino acid residue at a position corresponding to recited residues of SEQ ID NO: 47. By inserting the term "of SEQ ID NO: 47", Applicants have provided a reference sequence for the claimed amino acid substitutions as requested by the Examiner. Therefore, in light of the present amendment and for at least the reasons provided, it is submitted that this rejection is moot, and withdrawal of the rejection is respectfully requested.

II. Rejection Under 35 U.S.C. § 112, First Paragraph, Written Description

Claims 4-7 and 28-35 stand rejected under 35 U.S.C. § 112, first paragraph, as allegedly containing subject matter which was not described in the specification in such a way so to reasonably convey to one skill in the art that the inventors had possession of the claimed invention at the time the application was filed. *Id.* The Examiner alleges that "the functional definition of the claimed genus of engineered proteins does not provide any structural information commonly possessed by members of the genus which distinguish the protein species within the genus from other proteins such that one can visualize or recognize the identity of the members of the genus." *Id.* at page 4. Applicants respectfully disagree.

The genus of sequences encompassed by the presently amended claims is supported by Applicants' disclosure of common structural attributes.[1] Specifically, Applicants have provided a detailed chemical structure, *i.e.*, the substitution of at least one amino acid residue at a position corresponding to the recited residues of SEQ ID NO: 47. Furthermore, an engineered β-KAS protein falling within the scope of the present claims is readily recognizable based on the recited change in protein function with respect to the unaltered enzyme. The fact that an engineered β-KAS protein is comprised of additional residues is readily envisioned by one of ordinary skill in the art and disclosed throughout the present specification. Consequently, the present case is different from *Eli Lilly*. The present claims "distinguish the claimed invention from others" and define "structural features commonly possessed by members of the genus that distinguishes them from others," unlike the claims at issue in *Regents of the University of California v. Eli Lilly and Co.*, 119 F.3d 1559, 43 U.S.P.Q.2d 1398 (Fed. Cir. 1997).

The β-KAS protein family is described in the specification based on conserved protein structure and function. *See* specification at page 1, line 21 through page 2, line 11 (role of β-KAS proteins in the production of fatty acids); at page 2, lines 15-20 (inhibition by cerulenin); Figure 12 (conservation of amino acid sequence); and at page 5, line 24 through page 7, line 22 (conserved residues in the hydrophobic fatty

[1] Although Applicants disagree with the Examiner's rejections as applied to the non-amended claims, Applicants have amended the claims without prejudice. Please see Appendix A for a clean copy of all pending claims.

acid/cerulenin-binding pocket). An engineered β-KAS protein contains conserved residues that are specifically altered and protein function is correspondingly altered as a result of the specific amino acid mutations disclosed in the specification. The breadth of the claimed subject matter directly correlates to the broad scope of teaching on conservation of structure and function of particular amino acids disclosed in the specification. Therefore, Applicants have sufficiently described the claimed subject matter by structure and function.

The Examiner further alleges that "the disclosed species of mutant β-KAS proteins are insufficient to provided a representative number of species for adequate description of the claimed genus." Office Action mailed March 6, 2003 at page 4. Applicants respectfully disagree and point to Figure 12 in the specification. In Figure 12, a representative number of β-KAS protein sequences from plants, bacteria, mammals, and fungus are aligned based on amino acid sequence homology. Moreover, the claims recite a substitution of at least one amino acid residue at a position corresponding to recited residues of SEQ ID NO: 47. Read in light of the specification, an amino acid residue at a position corresponding to a recited residue of SEQ ID NO: 47 is clearly understood by the skilled artisan to identify a conserved amino acid relative to the *E. coli* β-KAS II sequence at the recited position. Accordingly, for at least the foregoing reasons, Applicants believe that the pending claims are fully described in the specification such that a skilled artisan would recognize that Applicants were in possession of the claimed invention. As such, the rejection under 35 U.S.C. §112, first paragraph, written description, is traversed and withdrawal of this rejection is respectfully requested.

III. Rejection Under 35 U.S.C. § 112, First Paragraph, Enablement

Claims 4-7 and 28-35 were rejected under 35 U.S.C. § 112, first paragraph, as not being enabled by the specification under an analysis of the factors presented in *In re Wands*, 858 F.2d 731, 737, 8 U.S.P.Q.2d 1400, 1404 (Fed. Cir. 1998). Office Action mailed March 6, 2003 at pages 4-6. The Examiner alleges that "[u]ndue experimentation would be required for a skilled artisan to make the entire scope of claimed beta-KAS II proteins." *Id.* at page 4.

Applicants respectfully disagree and assert that a reasonable analysis of the *In re Wands* criteria leads to the conclusion that undue experimentation is not required for a skilled artisan to make the entire scope of claimed engineered β-KAS proteins. Although Applicants disagree with the Examiner and traverse the rejection, the claims have been amended without prejudice to facilitate prosecution. As such, the following arguments are addressed with respect to the pending amended claims.

The last *Wands* criterion, and the one discussed first by the Examiner, focuses on the breadth of the claims. The Examiner acknowledges that the specification is enabling for amino acid substitutions at the recited positions where the engineered *E. coli* β-KAS II protein has the recited function. *See Id.* at page 5. However, the Examiner argues that the scope of the claims is "not commensurate with the enablement provided by the disclosure with regard to the extremely large number of engineered beta-KAS II proteins". *Id.* Applicants respectfully disagree.

Enablement is satisfied when the disclosure "adequately guide[s] the art worker to determine, without undue experimentation, which species among all those encompassed by the claimed genus possess the disclosed utility". *See In re Vaeck,* 947 F.2d 488, 496, 20 U.S.P.Q.2d 1438, 1445 (Fed. Cir. 1991). Here, enablement is satisfied because the art worker is guided by the disclosure to look, for example, to the conserved residues of a β-KAS protein family at a position corresponding to the recited amino acid residues of SEQ ID NO: 47. Further, the art worker is guided by the disclosure with respect to the rationale for making substitutions at the recited amino acids and the rationale for why the various substitutions have the recited effect. *See* specification at page 22, lines 10-29. Performing routine and well-known steps, such as sequence alignments and methods of mutating a given amino acid, cannot create undue experimentation even if it is laborious. *See In re Angstadt*, 537 F.2d 498, 504, 190 U.S.P.Q. 214, 218-219 (C.C.P.A. 1976). As such, the art worker is provided with the residue(s) for substitution and the effect of the substitution(s) on the engineered β-KAS protein with respect to the unaltered enzyme.

The third *Wands* criterion relates to the presence or absence of working examples. It is well established patent jurisprudence that Applicants need not teach "conventional and well-known genetic engineering techniques" (*see, for example, Ajinomoto Co. v.*

Archer-Daniels-Midland Co., 228 F.3d 1338, 1345, 56 U.S.P.Q.2d 1332, 1337 (Fed. Cir. 2000)). Furthermore, the Examiner acknowledged in the Office Action mailed June 26, 2002, that "methods of mutating a given amino acid sequence are well-known in the art". As stated previously, the specification provides, for example, identification and characterization of the β-KAS protein family, evidence of conservation of structure and function at specific amino acid residues, the crystal structure of *E. coli* β-KAS II binding to cerulenin (a ubiquitous inhibitor molecule of the β-KAS protein family), the engineered β-KAS protein sequences, the effects of the engineered β-KAS with respect to the native enzyme for both single and multiple substitutions, and provides data from the use of the claimed engineered β-KAS protein in a plant expression system. The numerous working examples provided in the specification represent a sufficient number of species to support the genus of engineered β-KAS proteins with specific mutations that result in specific changes in enzymatic activity. Based on the disclosure provided, mutations designed to alter the hydrophobic fatty acid/cerulenin binding pocket of *E. coli* β-KAS II (*e.g.* to widen, shorten, or lengthen the binding pocket) can predictably alter the substrate specificity of the enzyme. Because this binding pocket is highly conserved in the β-KAS protein family, the affects on enzyme activity, as demonstrated with numerous examples in *E. coli*, are expected in other members of the β-KAS protein family that have been engineered to have similar mutations in the conserved residues of the binding pocket.

The fifth and sixth *Wands* criteria focus on the state of the art and the relative skill in the art. The Examiner purports that the skilled artisan would have to test all possible combination of mutations to determine if said combination would result in a β-KAS protein with the desired activity. Office Action mailed March 6, 2003 at page 5. As stated previously, methods needed to make the engineered β-KAS proteins are known in the art as well as procedures to identify amino acid residues at a position corresponding to the recited residues of SEQ ID NO: 47. *See*, for example, Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor (1989), Mailga *et al.*, *Methods in Plant Molecular Biology*, Cold Spring Harbor (1995) and Birren *et al.*, *Genome Analysis: Analyzing DNA*, 1, Cold Spring Harbor (1997) and Haymes *et al.*, *Nucleic Acid Hybridization, A Practical Approach*, IRL Press, Washington, DC (1985). It is clear

from these resources that a person of ordinary skill in the art would be able to made and use the claimed engineered β-KAS proteins. Practitioners in this art have available to them considerable knowledge regarding how to align stretches of highly conserved sequences and an example of such as alignment is presented in Figure 12 of the specification. Therefore, the skilled artisan would be able to easily identify an amino acid residue of a β-KAS at a position corresponding to the recited residue of SEQ ID NO: 47 and make an appropriate substitution, as taught in the specification and working examples, for the desired, altered substrate specificity. Moreover, as stated above, the skilled artisan would expect a mutation in a conserved, functional region of a β-KAS protein to result in a similar activity as taught in the specification for *E. coli* β-KAS II.

The first *Wands* criterion is the quantity of experimentation necessary. As mentioned above, the "make-and-test" "quantum" of experimentation is reduced by the extensive knowledge, for example of conservative amino acid substitutions and sequence alignment parameters, to which a person of ordinary skill in the art has access. *See*, for example, the hybridization parameters set forth in Sambrook *et al.* (eds.), *Molecular Cloning: A Laboratory Manual*, 2d ed., pp. 9.47-11.61, Cold Spring Harbor Laboratory Press, Plainview, New York (1989) and Haymes *et al.*, *Nucleic Acid Hybridization, A Practical Approach*, IRL Press, Washington, D.C. (1985). Performing routine and well-known steps, such as sequence alignment protocols, molecular weight determination, and antibody hybridization assays, cannot create undue experimentation even if it is laborious. *See In re Angstadt*, 537 F.2d 498, 504, 190 U.S.P.Q. 214, 218-219 (C.C.P.A. 1976). Thus, the unaltered amino acids of a β-KAS protein that comprise a large portion of the claimed engineered β-KAS protein are rendered predictable to one of ordinary skill in the art. Furthermore, in light of the present disclosure there is more than a reasonable expectation of success that a substitution of an amino acid residue at a position corresponding to a recited residue of SEQ ID NO: 47 will result in the desired change in substrate specificity of a claimed engineered β-KAS protein.

The Examiner suggests that one skilled in the art would expect any tolerance to modification for a given protein to diminish with each further and additional modification. Office Action mailed March 6, 2003 at page 6. Applicants have tested the Examiner's prediction for β-KAS II in Figure 6, where the enzymatic activity for a 6:0-

ACP is reduced in the double mutants with respect to the corresponding single mutant. Accordingly in light of the specification, it is well within the ability of one skilled in the art to make or identify the claimed engineered β-KAS proteins and the results of the recited modifications.

The seventh *Wands* criterion considers the predictability of the art. The Examiner has presented no factual evidence why one of ordinary skill in the art would not be able to identify a β-KAS amino acid residue at a position corresponding to the recited residues of SEQ ID NO: 47 and make the amino acid residue substitutions for the desired change in substrate specificity. As discussed above, the specification provides sufficient guidance to one of skill in the art to decipher the information necessary to make and use the claimed engineered β-KAS proteins. Furthermore, the expectation that the desired change in substrate specificity of the unaltered enzyme will result is based, at least, on the conserved structure and function of the β-KAS protein family, the conserved structure and function of the hydrophobic fatty acid/cerulenin binding pocket in the β-KAS protein family, and the numerous working examples disclosing the ability of specific amino acid substitutions to alter the binding pocket and affect substrate specificity. The Examiner notes that a knowledge of and guidance with regard to which amino acids in the protein's sequence, if any, are tolerant of modification and which are conserved (i.e. expectedly intolerant to modification), and detailed knowledge of the ways in which the proteins' structure related to its function. Applicants have disclosed this detailed knowledge of structure and function in the specification and have further applied and proven their model for structure and function of the binding pocket by way, at least, of the working examples in the specification.[2]

The analysis of the *Wands* factors, discussed *supra*, establishes that one of ordinary skill in the art would be able to make and use the claimed engineered β-KAS proteins based on the disclosure in the specification. Furthermore, based on, at least, the

[2] Applicants respectfully direct the Examiner's attention to Figure 6, where the specific activity of 6:0-ACP is shown as greater than the wild-type activity. Applicants further direct the Examiner to page 6, lines 19-25 which refers to domain swapping between related β-KAS proteins, where extensive regions of the native β-KAS encoding sequence are replaced with the corresponding region from a different β-KAS.

conserved structure and function of the amino acid residues at positions corresponding to recited residues of SEQ ID NO: 47, the numerous working examples, and the rationale provided in the specification enable the full scope of the claimed subject matter. Accordingly, for at least these reasons, Applicants believe that the enablement rejection of claims 4-7 and 27-38 under 35 USC § 112, first paragraph, can not be sustained without specific, factual support from the Examiner. Reconsideration and withdrawal are respectfully requested.

Conclusion

In view of the foregoing amendments, Applicants believe that the application is in condition for allowance and solicit a Notice of Allowance indicating such at the earliest possible time. The Examiner is encouraged to contact the undersigned should any additional information be necessary.

Respectfully submitted,

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Appendix A

Claim 4 (**currently amended**) An engineered β-Ketoacyl-acyl carrier protein synthase protein comprising an amino acid sequence (i) wherein said amino acid sequence of said engineered β-Ketoacyl-acyl carrier protein synthase protein has a substitution of at least one amino acid residue selected from the group consisting of amino acid residues at a position corresponding to residue 108, 111, 114, 133, and 197 of SEQ ID NO: 47, and (ii) wherein said substitution is of a nonpolar side chain to a different nonpolar side chain, and (iii) wherein said engineered β-Ketoacyl-acyl carrier protein synthase protein increases long chain fatty acid accumulation compared to a β-Ketoacyl-acyl carrier protein synthase protein having at least one unaltered amino acid residue selected from the group consisting of amino acid residues at a position corresponding to residue 108, 111, 114, 133, and 197 of SEQ ID NO: 47.

Claim 5 (**currently amended**) The engineered β-Ketoacyl-acyl carrier protein synthase protein of claim 4, wherein said β-Ketoacyl-acyl carrier protein synthase protein is obtained from a prokaryotic source.

Claim 6 (**currently amended**) The engineered β-Ketoacyl-acyl carrier protein synthase protein of claim 4, wherein said β-Ketoacyl-acyl carrier protein synthase protein is obtained from *Escherichia coli*.

Claim 7 (**currently amended**) The engineered β-Ketoacyl-acyl carrier protein synthase protein claim 4, wherein said β-Ketoacyl-acyl carrier protein synthase protein is obtained from a plant source.

Claim 29 (**currently amended**) The engineered β-Ketoacyl-acyl carrier protein synthase protein of claim 4, wherein fatty acid production of said engineered β-Ketoacyl-acyl carrier protein synthase protein is altered such that short chain fatty acid accumulation is decreased compared to a β-Ketoacyl-acyl carrier protein synthase protein having said at least one unaltered residue.

Claim 30 (**currently amended**) An engineered β-Ketoacyl-acyl carrier protein synthase protein comprising an amino acid sequence (i) wherein said amino acid sequence of said engineered β-Ketoacyl-acyl carrier protein synthase protein has a substitution of at least one amino acid selected from the group consisting of amino acid residues at a position corresponding to residue 108 and 193 of SEQ ID NO: 47, and (ii) wherein said substitution is of a nonpolar side chain to a different nonpolar side chain, and (iii) wherein said engineered β-Ketoacyl-acyl carrier protein synthase protein preferentially accumulates fatty acids having a shorter chain length compared to a β-Ketoacyl-acyl carrier protein synthase protein having at least one unaltered amino acid residue selected from the group consisting of amino acid residues at a position corresponding to residue 108 and 193 of SEQ ID NO: 47.

Claim 31 (**currently amended**) The engineered β-Ketoacyl-acyl carrier protein synthase protein of claim 30, wherein said β-Ketoacyl-acyl carrier protein synthase protein is obtained from a prokaryotic source.

Claim 32 (**currently amended**) The engineered β-Ketoacyl-acyl carrier protein synthase protein of claim 30, wherein said β-Ketoacyl-acyl carrier protein synthase protein is obtained from *Escherichia coli*.

Claim 33 (**currently amended**) The engineered β-Ketoacyl-acyl carrier protein synthase protein of claim 30, wherein said β-Ketoacyl-acyl carrier protein synthase protein is obtained from a plant source.

Claim 34 (**currently amended**) The engineered β-Ketoacyl-acyl carrier protein synthase protein of claim 30, wherein fatty acid production of said engineered β-Ketoacyl-acyl carrier protein synthase protein is altered such that long chain fatty acid accumulation is decreased compared to a β-Ketoacyl-acyl carrier protein synthase protein having said at least one unaltered residue.

Claim 35 (**currently amended**) The engineered β-Ketoacyl-acyl carrier protein synthase protein of claim 30, wherein (i) said amino acid residue corresponding to the residue at position 108 of SEQ ID NO: 47 is selected from the group consisting of isoleucine, leucine, and methionine and wherein (ii) said amino acid residue is substituted with phenylalanine.

Claim 36 (**currently amended**) The engineered β-Ketoacyl-acyl carrier protein synthase protein of claim 30, wherein (i) said amino acid residue corresponding to the residue at position 108 of SEQ ID NO: 47 is selected from the group consisting of isoleucine and methionine and wherein (ii) said amino acid residue is substituted with leucine.

Claim 37 (**currently amended**) The engineered β-Ketoacyl-acyl carrier protein synthase protein of claim 30, wherein (i) said amino acid residue corresponding to the residue at position 193 of SEQ ID NO: 47 is selected from the group consisting of alanine, phenylalanine, valine, and leucine and wherein (ii) said amino acid residue is substituted with isoleucine.

Claim 38 (**currently amended**) The engineered β-Ketoacyl-acyl carrier protein synthase protein of claim 30, wherein (i) said amino acid residue corresponding to the residue at position 193 of SEQ ID NO: 47 is selected from the group consisting of alanine, phenylalanine, valine, and leucine and wherein (ii) said amino acid residue is substituted with methionine.

Claim 39 (**new**) The engineered β-Ketoacyl-acyl carrier protein synthase protein of claim 4, wherein (i) said amino acid residue corresponding to the residue at position 108 of SEQ ID NO: 47 is selected from the group consisting of alanine, valine, leucine, isoleucine, and methionine, and wherein (ii) said amino acid residue is substituted with alanine.

Claim 40 (**new**) The engineered β-Ketoacyl-acyl carrier protein synthase protein of claim 4, wherein (i) said amino acid residue corresponding to the residue at position 111 of SEQ ID NO: 47 is selected from the group consisting of phenylalanine, isoleucine, and leucine, and wherein (ii) said amino acid residue is substituted with alanine.

Claim 41 (**new**) The engineered β-Ketoacyl-acyl carrier protein synthase protein of claim 4, wherein (i) said amino acid residue corresponding to the residue at position 114 of SEQ ID NO: 47 is selected from the group consisting of alanine, valine, leucine, isoleucine, and methionine, and wherein (ii) said amino acid residue is substituted with alanine.

Claim 42 (**new**) The engineered β-Ketoacyl-acyl carrier protein synthase protein of claim 4, wherein (i) said amino acid residue corresponding to the residue at position 133 of SEQ ID NO: 47 is selected from the group consisting of phenylalanine and isoleucine, and leucine and wherein (ii) said amino acid residue is substituted with alanine.

Claim 43 (**new**) The engineered β-Ketoacyl-acyl carrier protein synthase protein of claim 4, wherein (i) said amino acid residue corresponding to the residue at position 197 of SEQ ID NO: 47 is selected from the group consisting of leucine and isoleucine and wherein (ii) said amino acid residue is substituted with alanine.

Claim 44 (**new**) The engineered β-Ketoacyl-acyl carrier protein synthase protein of claim 4, wherein said engineered β-Ketoacyl-acyl carrier protein synthase protein accumulates normal membrane components compared to a β-Ketoacyl-acyl carrier protein synthase protein having said at least one unaltered residue.

Claim 45 (**new**) The engineered β-Ketoacyl-acyl carrier protein synthase protein of claim 4, wherein said engineered β-Ketoacyl-acyl carrier protein synthase protein accumulates longer than normal membrane components compared to a β-Ketoacyl-acyl carrier protein synthase protein having said at least one unaltered residue.

Claim 46 (**new**) The engineered β-Ketoacyl-acyl carrier protein synthase protein of claim 4, wherein said engineered β-Ketoacyl-acyl carrier protein synthase protein is more specific for the synthesis of eight carbon fatty acids compared to a β-Ketoacyl-acyl carrier protein synthase protein having said at least one unaltered residue.

Claim 47 (**new**) The engineered β-Ketoacyl-acyl carrier protein synthase protein of claim 4, wherein said engineered β-Ketoacyl-acyl carrier protein synthase protein (i) has an alanine substitution at positions corresponding to residues 108, 111, and 114 of SEQ ID NO: 47 and (ii) wherein said engineered β-Ketoacyl-acyl carrier protein synthase protein synthesizes longer carbon chain fatty acids in transgenic plants compared to wild-type plants.

Claim 48 (**new**) The engineered β-Ketoacyl-acyl carrier protein synthase protein of claim 4, wherein said engineered β-Ketoacyl-acyl carrier protein synthase protein (i) has an alanine substitution at positions corresponding to residues 108, 111, and 114 of SEQ ID NO: 47 and (ii) wherein said engineered β-Ketoacyl-acyl carrier protein synthase protein synthesizes longer carbon chain fatty acids in transgenic plants compared to a β-Ketoacyl-acyl carrier protein synthase protein having said at least one unaltered residue in transgenic plants.

Claim 49 (**new**) The engineered β-Ketoacyl-acyl carrier protein synthase protein of claim 4, wherein said engineered β-Ketoacyl-acyl carrier protein synthase protein (i) has an alanine substitution at positions corresponding to residues 108, 111, 114, 133, 197 of SEQ ID NO: 47 and (ii) wherein said engineered β-Ketoacyl-acyl carrier protein synthase protein synthesizes longer carbon chain fatty acids in transgenic plants compared to wild-type plants.

Claim 50 (**new**) The engineered β-Ketoacyl-acyl carrier protein synthase protein of claim 4, wherein said engineered β-Ketoacyl-acyl carrier protein synthase protein (i) has an alanine substitution at positions corresponding to residues 108, 111, 114, 133, 197 of SEQ ID NO: 47 and (ii) wherein said engineered β-Ketoacyl-acyl carrier protein synthase protein synthesizes longer carbon chain fatty acids in transgenic plants compared to a β-Ketoacyl-acyl carrier protein synthase protein having said at least one unaltered residue in transgenic plants.

Claim 51 (**new**) The engineered β-Ketoacyl-acyl carrier protein synthase protein of claim 30, wherein said engineered β-Ketoacyl-acyl carrier protein synthase protein has a reduced abilitity to utilize C8-ACP and longer substrates for condensation while still able to use the C6-ACP for elongation to produce C8 fatty acids.

Claim 52 (**new**) The engineered β-Ketoacyl-acyl carrier protein synthase protein of claim 30, wherein said engineered β-Ketoacyl-acyl carrier protein synthase protein has an increased ability to utilize C6-ACP substrates for elongation compared to a β-Ketoacyl-acyl carrier protein synthase protein having said at least one unaltered residue.

Claim 53 (**new**) An engineered β-Ketoacyl-acyl carrier protein synthase protein comprising an amino acid sequence (i) wherein said amino acid sequence of said engineered β-Ketoacyl-acyl carrier protein synthase protein has a substitution of at least one amino acid residue selected from the group consisting of amino acid residues at a position corresponding to residue 108, 134, 193, 202 and 342 of SEQ ID NO: 47, and (ii) wherein said substitution is of a nonpolar side chain to a smaller nonpolar side chain, and (iii) wherein said engineered β-Ketoacyl-acyl carrier protein synthase protein has an altered elongator molecule preference compared to a β-Ketoacyl-acyl carrier protein synthase protein having at least one unaltered amino acid residue selected from the group consisting of amino acid residues at a position corresponding to residue 108, 134, 193, 202 and 342 of SEQ ID NO: 47.

Claim 54 (**new**) The engineered β-Ketoacyl-acyl carrier protein synthase protein of claim 53, wherein said β-Ketoacyl-acyl carrier protein synthase protein is obtained from a prokaryotic source.

Claim 55 (**new**) The engineered β-Ketoacyl-acyl carrier protein synthase protein of claim 53, wherein said β-Ketoacyl-acyl carrier protein synthase protein is obtained from *Escherichia coli*.

Claim 56 (**new**) The engineered β-Ketoacyl-acyl carrier protein synthase protein of claim 53, wherein said β-Ketoacyl-acyl carrier protein synthase protein is obtained from a plant source.

Claim 57 (**new**) The engineered β-Ketoacyl-acyl carrier protein synthase protein of claim 53, wherein said elongator molecule is a molecule other than Malonyl-ACP.

Claim 58 (**new**) The amino acid sequence of claim 53, wherein said engineered β-Ketoacyl-acyl carrier protein synthase protein produces a branched chained fatty acid.

Claim 59 (**new**) The engineered β-Ketoacyl-acyl carrier protein synthase protein of claim 53, wherein (i) said amino acid residue corresponding to the residue at position 108 of SEQ ID NO: 47 is selected from the group consisting of alanine, valine, leucine, isoleucine, and methionine, and wherein (ii) said amino acid residue is substituted with glycine.

Claim 60 (**new**) The engineered β-Ketoacyl-acyl carrier protein synthase protein of claim 53, wherein (i) said amino acid residue corresponding to the residue at position 134 of SEQ ID NO: 47 is selected from the group consisting of valine and isoleucine and wherein (ii) said amino acid residue is substituted with glycine.

Claim 61 (**new**) The engineered β-Ketoacyl-acyl carrier protein synthase protein of claim 53, wherein (i) said amino acid residue corresponding to the residue at position 134 of SEQ ID NO: 47 is selected from the group consisting of valine and isoleucine and wherein (ii) said amino acid residue is substituted with alanine.

Claim 62 (**new**) The engineered β-Ketoacyl-acyl carrier protein synthase protein of claim 53, wherein (i) said amino acid residue corresponding to the residue at position 193 of SEQ ID NO: 47 is selected from the group consisting of alanine, phenylalanine, valine, and leucine and wherein (ii) said amino acid residue is substituted with glycine.

Claim 63 (**new**) The engineered β-Ketoacyl-acyl carrier protein synthase protein of claim 53, wherein (i) said amino acid residue corresponding to the residue at position 202 of SEQ ID NO: 47 is a phenylalanine and wherein (ii) said phenylalanine is substituted with an amino acid residue selected from the group consisting of isoleucine, leucine, and glycine.

Claim 64 (**new**) The engineered β-Ketoacyl-acyl carrier protein synthase protein of claim 53, wherein (i) said amino acid residue corresponding to the residue at position 342 of SEQ ID NO: 47 is a leucine and wherein (ii) said leucine is substituted with an amino acid residue selected from the group consisting of alanine and glycine.